AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

Claims 1-24. (cancelled)

25. (new) A method of genotyping HCV present in a biological sample comprising the steps of

hybridizing nucleic acids in the biological sample with a collection of probes, and

detecting one or more complexes formed between said probes and said nucleic acids of HCV,

wherein said collection of probes is capable of genotyping at least three genotypes of HCV, and wherein said collection of probes hybridizes to the 5' untranslated region of HCV.

26. (new) The method according to claim 25, wherein said collection is capable of genotyping at least four genotypes of HCV.

27. (new) The method according to claim 25, wherein said collection is capable of genotyping at least five genotypes of HCV.

28. (new) The method according to claim 25, wherein said collection is capable of genotyping at least six genotypes of HCV.

29. (new) The method according to any of claims 25-28, wherein said collection is also capable of sub-typing at least four sub-types of HCV.

30. (new) The method according to any of claims 25-28, wherein said collection is also capable of sub-typing at least eight sub-types of HCV.

31. (new) The method according to any of claims 25-28, wherein said collection is also capable of sub-typing at least twelve sub-types of HCV.

32. (new) The method according to any of claims 25-28, wherein said collection is also capable of sub-typing at least sixteen sub-types of HCV.

33. (new) The method according to any of claims 25-28, wherein the collection comprises at least two probes that specifically hybridize with at least one pair of domains selected from the group of domain pairs consisting of:

one domain extending from nucleotide at position -170 to nucleotide at position -155 and the other domain extending from nucleotide at position -141 to nucleotide at position -117,

one domain extending from nucleotide at position -170 to nucleotide at position -155 and the other domain extending from nucleotide position -103 to nucleotide at position -88,

one domain extending from nucleotide at position -141 to nucleotide at position -117 and the other domain extending from nucleotide position at -103 to nucleotide at position -88,

one domain extending from nucleotide at position -170 to nucleotide at position -155 and the other domain extending from nucleotide position at -83 to nucleotide at position -68,

one domain extending from nucleotide at position -141 to nucleotide at position -117 and the other domain extending from nucleotide position at -83 to nucleotide at position -68,

one domain extending from nucleotide at position -170 to nucleotide at position -155 and the other domain extending from nucleotide position at -146 to nucleotide at position -130,

one domain extending from nucleotide at position -146 to nucleotide at position -130 and the other domain extending from nucleotide position at -132 to nucleotide at position -117, and

one domain extending from nucleotide at position -146 to nucleotide at position -130 and the other domain extending from nucleotide position at -103 to nucleotide at position -88, with said negative numbering of the nucleotide positions starting at the nucleotide preceding the first ATG codon of the open reading frame encoding the HCV polyprotein.

34. (new) The method according to claim 33, wherein the collection comprises at least two sets of probes, each set comprising at least two probes, and wherein each set

of probes specifically hybridizes with a different pair of domains selected from the recited groups of domain pairs.

35. (new) The method according to claim 33, wherein the collection comprises at least three sets of probes, each set comprising at least two probes, and wherein each set of probes specifically hybridizes with a different pair of domains selected from the recited groups of domain pairs.

36. (new) The method according to claim 33, wherein the collection comprises at least four sets of probes, each set comprising at least two probes, and wherein each set of probes specifically hybridizes with a different pair of domains selected from the recited groups of domain pairs.

37. (new) The method according to any of claims 25-28, wherein at least two of said probes specifically hybridize to the domain extending from the nucleotides at positions -291 to -66 of the 5' untranslated region of HCV.

38. (new) The method according to claims 25-28, wherein at least one of said probes specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the group consisting of

(a) the one extending from nucleotide at position -293 to nucleotide at position -278,

(b) the one extending from nucleotide at position -275 to nucleotide at position -260,

(c) the one extending from nucleotide at position -253 to nucleotide at position -238,

(d) the one extending from nucleotide at position -244 to nucleotide at position -229,

(e) the one extending from nucleotide at position -238 to nucleotide at position -223,

(f) the one extending from nucleotide at position -170 to nucleotide at position -155,

(g) the one extending from nucleotide at position -141 to nucleotide at position -117,

(h) the one extending from nucleotide at position -83 to nucleotide at position -68,

(i) the one extending from nucleotide at position -103 to nucleotide at position -88, and

(j) the one extending from nucleotide at position -146 to nucleotide at position -130.

wherein said collection comprises at least two probes, each of which specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the recited group of domains, and wherein the two probes specifically hybridize to different domains selected from the recited group of domains.

39. (new) The method according to claim 38, wherein said collection comprises at least three probes, each of which specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the recited group of domains, and wherein the three probes specifically hybridize to different domains selected from the recited group of domains.

40. (new) The method according to claim 39, wherein said collection comprises at least four probes, each of which specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the recited group of domains, and wherein the four probes specifically hybridize to different domains selected from the recited group of domains.

41. (new) The method according to claim 40, wherein said collection comprises at least five probes, each of which specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the recited group of domains, and wherein the five probes specifically hybridize to different domains selected from the recited group of domains.

42. (new) The method according to claim 41, wherein said collection comprises at least six probes, each of which specifically hybridizes to at least 5 contiguous nucleotides in a domain selected from the recited group of domains, and wherein the six probes specifically hybridize to different domains selected from the recited group of domains.

43. (new) The method according to any of claims 25-28, wherein said collection is capable of genotyping HCV genotypes selected from the group consisting of HCV type 1, HCV type 2, HCV type 3, HCV type 4, HCV type 5, and HCV type 6.

44. (new) The method according to any of claims 25-28, wherein at least one probe hybridizes to at least one of the domains selected from the group consisting of

for HCV type 1 and 6: AAT TGC CAG GAC GAC C (SEQ ID NO: 5), TCT CCA GGC ATT GAG C (SEQ ID NO: 6), ATT TGC CAG GAY GAC C (SEQ ID NO: 28),

for HCV type 1: GCT CAG TGC CTG GAG A (SEQ ID NO: 29),

for HCV type 2: TAG CGT TGG GTT GCG A (SEQ ID NO: 8), TTR CCG GRA AGA CTG G (SEQ ID NO: 9), TGR CCG GGC ATA GAG T (SEQ ID NO: 10), TTA CCG GGA AGA CTG G (SEQ ID NO: 11), TGA CCG GAC ATA GAG T (SEQ ID NO: 12), CGT ACA GCC TCC AGG C (SEQ ID NO: 32), CCG GGA AGA CTG GGT C (SEQ ID NO: 22), CCG GAA AGA CTG GGT C (SEQ ID NO: 23), ACC CAC TCT ATG CCC G (SEQ ID NO: 24), ACC CAC TCT ATG TCC G (SEQ ID NO: 25), ATA GAG TGG GTT TAT C (SEQ ID NO: 26), GGA CCC AGT CTT CTT G (SEQ ID NO: 33), TGC CTG GTC ATT TGG G (SEQ ID NO: 34),

for HCV type 3: AAT CGC TGG GGT GAC C (SEQ ID NO: 13), TTT CTG GGT ATT GAG C (SEQ ID NO: 14), CCG CGA GAT CAC TAG C (SEQ ID NO: 21), CCG CAA GAT CAC TAG C (SEQ ID NO: 36), GAA TCG CCG GGT TGA C (SEQ ID NO: 54),

for HCV type 4 and 5: AAT YGC CGG GAT GAC C (SEQ ID NO: 17),

for HCV type 4: TTC TTG GAA CTA ACC C (SEQ ID NO: 18),

for HCV type 4, 3c & 3b: TTT CCG GGC ATT GAG C (SEQ ID NO: 19),

for HCV type 4 and 3b: ATT CGC CGG GAT GAC C (SEQ ID NO: 38),

for HCV type 4: GAG TGT TGT ACA GCC T (SEQ ID NO: 37), GAG TGT TGT GCA GCC T (SEQ ID NO: 39), AAT CGC CGG GAC GAC C (SEQ ID NO: 40), AAT GCC CGG CAA TTT G (SEQ ID NO: 41), AAT CGC CGA GAT GAC C (SEQ ID NO: 42), AAT GCT CGG AAA TTT G (SEQ ID NO: 43), AAT CGC CAG GAT GAC C (SEQ ID NO: 49), TGC CTG GAA ATT TGG G (SEQ ID NO: 50), GGA ATC GCC AGG ACG A (SEQ ID NO: 53),

for HCV type 5: AAT TGC CGG GAT GAC C (SEQ ID NO: 45), AAT TGC CGG GAC GAC C (SEQ ID NO: 47), TCT CCG GGC ATT GAG C (SEQ ID NO: 46), GAG TGT CGA ACA GCC T (SEQ ID NO: 44),

for HCV type 6: GGG TCC TTT CCA TTG G (SEQ ID NO: 48), and

domains fully complementary to all of the above sequences, wherein Y is C or T, and K is G or T, and wherein T is replaced by U.

45. (new) The method according to claim 44, wherein at least two probes hybridize to domains selected from the recited group, and wherein the at least two probes hybridize to different domains.

46. (new) The method according to claim 45, wherein at least three probes hybridize to domains selected from the recited group, and wherein the at least three probes hybridize to different domains.

47. (new) The method according to claim 46, wherein at least four probes hybridize to domains selected from the recited group, and wherein the at least four probes hybridize to different domains.

48. (new) The method according to any of claims 25-28, wherein said collection comprises at least one probe which can be used for detecting the presence of HCV type 6.

49. (new) The method according to claim 48, wherein, wherein said at least one probe hybridizes to the domain of:

GGG TCC TTT CCA TTG G (SEQ ID NO:48)

or a domain fully complementary to the above sequence.

50. (new) The method according to any of claims 25-28, wherein said collection comprises a mixture or two or more probes.

51. (new) The method according to claim 50, wherein said collection comprises a mixture or three or more probes.

52. (new) The method according to claims 25-28, wherein said collection of probes is contained in a kit.

53. (new) The method according to claim 52, wherein said collection comprises a mixture or two or more probes.

54. (new) The method according to claim 52, wherein said collection comprises a mixture or three or more probes.

55. (new) The method according to claim 52, wherein the collection of probes is immobilized to a solid support.

56. (new) The method according to claim 53, wherein the collection of probes is immobilized to a solid support.

57. (new) The method according to claim 54, wherein the collection of probes is immobilized to a solid support.

58. (new) A method of detecting the presence of HCV type 6 present in a biological sample comprising the steps of

hybridizing nucleic acids in the biological sample with at least one probe, and

detecting one or more complexes formed between at least said one probe and said nucleic acids of HCV,

wherein said at least one probe is capable of hybridizing to a HCV type 6 specific sequence in the 5' untranslated region of HCV.

59. (new) A method of detecting the presence of HVC type 6 according to claim 58, wherein the at least one probe hybridizes to the domain of:

GGG TCC TTT CCA TTG G (SEQ ID NO:48)

or a domain fully complementary to the above sequence.